

Sequen-	US-10-502-441-4	AAV0638
ce:	5901	Aav28401
Effect score:	1 MTRAPRCPAVSLLESRYRE.....TILKAAADPALSTDQTILD 1122	Human EST
Influence:		Aay95566 hEST2, a
String table:	BLOSUM62	Adc47061 Human TER
Gapopen:	10.0 , Gapext: 0.5	Ade40482 Human tel
Searched:	2443163 seqs, 439378781 residues	Aas38666 Human tel
All number of hits satisfying chosen parameters:	2443163	Aaw6113 Human tel
		Aaw6113 Glutathione S-transferase
		Aay0647 Telomeras
		Aaw56101 Enhanced
		Aav0641 telomeras

maximum DB sea length: 0

t-processing: Minimum Match 0% Maximum Match 100% Filtering First 45 summaries

AY26579; 13-SEP-1999 (first entry)
Murine telomerase reverse transcriptase (mTERT) enzyme.
Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
immunogen; enzyme; telomerase-mediated DNA replication.

No. is the number of results predicted by chance to have a score greater than or equal to the score of the test being printed, and is derived by analysis of the total score distribution.

NUMERICS

Query ID	Score	Match Length	DB ID	Description	
				Start	End
1	5901	100.0	11122	2	AAY26579
2	5901	100.0	11122	8	ADG99601
3	5854	99.2	11122	5	ADG96711
4	4859	82.3	11152	8	ADG96069
5	4751	80.5	11128	7	ADD21416
6	4751	80.5	11128	8	ADG91603
7	3505	59.4	11132	2	AAW4957
8	3505	59.4	11132	2	AAW9251
9	3505	59.4	11132	2	AAW92881
10	3505	59.4	11132	2	AAY30090
11	3505	59.4	11132	2	AAY41621
12	3505	59.4	11132	2	AAY25580
13	3505	59.4	11132	4	AAG61859
14	3505	59.4	11132	4	AAG61329
15	3505	59.4	11132	4	AAB9930
16	3505	59.4	11132	4	AAB8765
17	3505	59.4	11132	5	AEE2226
18	3505	59.4	11132	5	AAU7235
19	3505	59.4	11132	6	ABR4384
20	3505	59.4	11132	6	ABR4063
21	3505	59.4	11132	6	ABP5676
22	3505	59.4	11132	6	ABR5045
23	3505	59.4	11132	7	ADD14240
24	3505	59.4	11132	7	ADH77243
					Human tel
					Murine tel
					Murine TE
					AddG99601
					Mouse tel
					ADG96069
					TERT cons
					Golden ha
					Add21416
					Hamster T
					Aaw4957
					Human tel
					Aaw9251
					Human cat
					Aay2881
					Human tel
					Aay30090
					Aay41621
					Aay25580
					Aag61859
					Heart mus
					Aag61329
					Human pro
					Aab9930
					Human tel
					Aab8765
					Human tel
					Aee2226
					Human tel
					Aau7235
					Human tel
					Abr4384
					Human tel
					Abr4063
					Human tel
					Abp5676
					Human tel
					ABR5045
					Human tel
					Add214240
					Human TCR

25-NOV-1998; 98WO-US25211.
26-NOV-1997; 97US-00979742.
16-MAR-1998; 98US-0042460.

(GERO-) GERON CORP.
(YESH) UNIV YESHIVA EINSTEIN COLLEGE.
Morin GB, Allsopp R, Depinho R, Greenberg R;
WPI; 1999-347722/29.
N-PSDB; AAX80994.

Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and nucleic acids.

Claim 8; Fig 2; 135pp; English.

The invention relates to a mouse telomerase reverse transcriptase ($mTERT$) enzyme. Compositions containing $mTERT$ can be used in telomere length assays. Isolated $mTERT$ is useful as an immunogen for the production of monoclonal or polyclonal antibodies. The method is useful for assessing the degree of purification and identification of new $mTERT$ species, such as an $mTERT$ allele, homolog or isoform, or to screen for modulators (antagonists and agonists) of telomerase-mediated DNA replication. Antagonists and agonists of $mTERT$ can be used to modify the activity of other telomerase enzymes such as human TERT ($hTERT$). The present sequence represents a $mTERT$ enzyme.

XX	Sequence 1122 AA;								
SQ	Query Match 100.0%; Score 5901; DB 2; Length 1122;	Qy	Best Local Similarity 100.0%; Pred. No. 0; Matches 1122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	Db 961 KTMRNKLLSVTRLKCHGLPFDLQVNLSLQTVICINIVKIFLQAYRFAHCYVQLPPDQRVRK 1020	Qy	Qy 1021 NLTFPLGIISSQASCCYATIILKUNQNGMTLKASGSPPPEAHMLCYQAFJLKAHSVYK 1080	Db	Db 1021 NLTFPLGIISSQASCCYATIILKUNQNGMTLKASGSPPPEAHMLCYQAFJLKAHSVYK 1080
Qy	1 MTRAPCPAVRSLLRSRYEWTPLATFVRRIGPEGRRLVQPGDPKTYRTLVQAOLVCMW 60	Db	Db 1 MTRAPCPAVRSLLRSRYEWTPLATFVRRIGPEGRRLVQPGDPKTYRTLVQAOLVCMW 60	Qy	Qy 1081 CLLGFLRTAQKLCKRLPKATMTLKAADPASTDQTILD 1122	Db	Db 1081 CLLGFLRTAQKLCKRLPKATMTLKAADPASTDQTILD 1122	Qy	Qy 1081 CLLGFLRTAQKLCKRLPKATMTLKAADPASTDQTILD 1122
Db	RESULT 2 ADG90601 standard; protein; 1122 AA.	Qy	61 GSOPPPADLSPHQVSSILKELYARVYORLCEERNENVLAFGFELLNEARGGPMAPTSSR 120	Db	Db 61 GSOPPPADLSPHQVSSILKELYARVYORLCEERNENVLAFGFELLNEARGGPMAPTSSR 120	Qy	Qy 121 SYLPNTVETURVGAMMILLSRGDDLVYLALLAHCALYLLVPPSCAYQVCGSPLYQICA 180	Db	Db 121 SYLPNTVETURVGAMMILLSRGDDLVYLALLAHCALYLLVPPSCAYQVCGSPLYQICA 180
Qy	121 SYLPNTVETURVGAMMILLSRGDDLVYLALLAHCALYLLVPPSCAYQVCGSPLYQICA 180	Db	Db 121 SYLPNTVETURVGAMMILLSRGDDLVYLALLAHCALYLLVPPSCAYQVCGSPLYQICA 180	Qy	Qy 181 TTDIWPSVASYRTRPVRGFTNLRPLQQIKKSROEAPKPLAPSRTGKRHLSLTSTS 240	Db	Db 181 TTDIWPSVASYRTRPVRGFTNLRPLQQIKKSROEAPKPLAPSRTGKRHLSLTSTS 240	Qy	Qy 181 TTDIWPSVASYRTRPVRGFTNLRPLQQIKKSROEAPKPLAPSRTGKRHLSLTSTS 240
Db	mouse; immune response; telomerase reverse transcriptase; TERT; cytostatic; immunostimulant; cancer; cytotoxic T cell response.	Qy	181 TTDIWPSVASYRTRPVRGFTNLRPLQQIKKSROEAPKPLAPSRTGKRHLSLTSTS 240	Db	Db 181 TTDIWPSVASYRTRPVRGFTNLRPLQQIKKSROEAPKPLAPSRTGKRHLSLTSTS 240	Qy	Qy 241 VPSAKKRCRCPYPRVPRGPHQVLPPSGKSWVPSPARSPEVPTAEDLSSKGKVSDLSL 300	Db	Db 241 VPSAKKRCRCPYPRVPRGPHQVLPPSGKSWVPSPARSPEVPTAEDLSSKGKVSDLSL 300
Qy	241 VPSAKKRCRCPYPRVPRGPHQVLPPSGKSWVPSPARSPEVPTAEDLSSKGKVSDLSL 300	Db	Db 241 VPSAKKRCRCPYPRVPRGPHQVLPPSGKSWVPSPARSPEVPTAEDLSSKGKVSDLSL 300	Qy	Qy 301 SGSVCCRKHPSTSSTLSPRONAFQRLPIERFLYSPRGQERLNPSFLSNIQPNLT 360	Db	Db 301 SGSVCCRKHPSTSSTLSPRONAFQRLPIERFLYSPRGQERLNPSFLSNIQPNLT 360	Qy	Qy 301 SGSVCCRKHPSTSSTLSPRONAFQRLPIERFLYSPRGQERLNPSFLSNIQPNLT 360
Db	08-JAN-2004.	Db	Db 301 SGSVCCRKHPSTSSTLSPRONAFQRLPIERFLYSPRGQERLNPSFLSNIQPNLT 360	Qy	Qy 361 GARRLYEVITIPLGSRPTSGLPCRTHRLSRRYQMRPLFQQLVNHAEQCTYRLJRSHCRP 420	Db	Db 361 GARRLYEVITIPLGSRPTSGLPCRTHRLSRRYQMRPLFQQLVNHAEQCTYRLJRSHCRP 420	Qy	Qy 361 GARRLYEVITIPLGSRPTSGLPCRTHRLSRRYQMRPLFQQLVNHAEQCTYRLJRSHCRP 420
Qy	24-JUN-2003; 2003W0-US019844.	Db	Db 361 GARRLYEVITIPLGSRPTSGLPCRTHRLSRRYQMRPLFQQLVNHAEQCTYRLJRSHCRP 420	Qy	Qy 421 RTANOOVTDALNTSPPHMDLIRLHSSPPOVYGGPLBACLKVKVSAASLWGTGRHNERFFKVN 480	Db	Db 421 RTANOOVTDALNTSPPHMDLIRLHSSPPOVYGGPLBACLKVKVSAASLWGTGRHNERFFKVN 480	Qy	Qy 421 RTANOOVTDALNTSPPHMDLIRLHSSPPOVYGGPLBACLKVKVSAASLWGTGRHNERFFKVN 480
Db	PA 27-JUN-2002; 2002US-0393295P.	Db	Db 421 RTANOOVTDALNTSPPHMDLIRLHSSPPOVYGGPLBACLKVKVSAASLWGTGRHNERFFKVN 480	Qy	Qy 481 LKKFISIGKYGKLSQELMWKVKVEDCHWLSSPGKDRPVAEHLRERLATELFWLM 540	Db	Db 481 LKKFISIGKYGKLSQELMWKVKVEDCHWLSSPGKDRPVAEHLRERLATELFWLM 540	Qy	Qy 481 LKKFISIGKYGKLSQELMWKVKVEDCHWLSSPGKDRPVAEHLRERLATELFWLM 540
Qy	PA (GERO-) GERON CORP.	Db	Db 481 LKKFISIGKYGKLSQELMWKVKVEDCHWLSSPGKDRPVAEHLRERLATELFWLM 540	Qy	Qy 541 TYVQQLRSRFFYTESTFQQRFLIFFYTKSYWSKLSQSIGVROLERYLRELQSSEVRHQ 600	Db	Db 541 TYVQQLRSRFFYTESTFQQRFLIFFYTKSYWSKLSQSIGVROLERYLRELQSSEVRHQ 600	Qy	Qy 481 LKKFISIGKYGKLSQELMWKVKVEDCHWLSSPGKDRPVAEHLRERLATELFWLM 540
Db	XX	Db	Db 541 TYVQQLRSRFFYTESTFQQRFLIFFYTKSYWSKLSQSIGVROLERYLRELQSSEVRHQ 600	Qy	Qy 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660	Db	Db 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660	Qy	Qy 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660
Qy	CC	Db	Db 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660	Qy	Qy 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660	Db	Db 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660	Qy	Qy 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660
Db	CC	Db	Db 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660	Qy	Qy 661 KPHLIMCSVSIGMDITRTRAPFLVRAALQTPRMVFKADTVGAYDA.PQGKLVVEWA 720	Db	Db 661 KPHLIMCSVSIGMDITRTRAPFLVRAALQTPRMVFKADTVGAYDA.PQGKLVVEWA 720	Qy	Qy 661 KPHLIMCSVSIGMDITRTRAPFLVRAALQTPRMVFKADTVGAYDA.PQGKLVVEWA 720
Qy	CC	Db	Db 661 KPHLIMCSVSIGMDITRTRAPFLVRAALQTPRMVFKADTVGAYDA.PQGKLVVEWA 720	Qy	Qy 721 NMIRHSESTYCIROVAVRDRSQQGTHSKFSERQVTTLSDLOPMGOFKLHQDSASLR 780	Db	Db 721 NMIRHSESTYCIROVAVRDRSQQGTHSKFSERQVTTLSDLOPMGOFKLHQDSASLR 780	Qy	Qy 721 NMIRHSESTYCIROVAVRDRSQQGTHSKFSERQVTTLSDLOPMGOFKLHQDSASLR 780
Db	CC	Db	Db 721 NMIRHSESTYCIROVAVRDRSQQGTHSKFSERQVTTLSDLOPMGOFKLHQDSASLR 780	Qy	Qy 781 NSVVIQOSISHNESSSSLEDFPLHLRHSVYKIGDRCYTOCGIPQGSLSLICSLCFG 840	Db	Db 781 NSVVIQOSISHNESSSSLEDFPLHLRHSVYKIGDRCYTOCGIPQGSLSLICSLCFG 840	Qy	Qy 781 NSVVIQOSISHNESSSSLEDFPLHLRHSVYKIGDRCYTOCGIPQGSLSLICSLCFG 840
Qy	CC	Db	Db 781 NSVVIQOSISHNESSSSLEDFPLHLRHSVYKIGDRCYTOCGIPQGSLSLICSLCFG 840	Qy	Qy 841 DMENKLPAEVQRDGLLRFVDDFLUTPHDOAKTFLSTLVHGVPYGMCNLQKTVNF 900	Db	Db 841 DMENKLPAEVQRDGLLRFVDDFLUTPHDOAKTFLSTLVHGVPYGMCNLQKTVNF 900	Qy	Qy 841 DMENKLPAEVQRDGLLRFVDDFLUTPHDOAKTFLSTLVHGVPYGMCNLQKTVNF 900
Db	CC	Db	Db 841 DMENKLPAEVQRDGLLRFVDDFLUTPHDOAKTFLSTLVHGVPYGMCNLQKTVNF 900	Qy	Qy 901 PVEPGTIGGAAYQLPAHCLPWCGLULLDTOTLEYCDSYGAQTSIKTSATFQSYFKAG 960	Db	Db 901 PVEPGTIGGAAYQLPAHCLPWCGLULLDTOTLEYCDSYGAQTSIKTSATFQSYFKAG 960	Qy	Qy 901 PVEPGTIGGAAYQLPAHCLPWCGLULLDTOTLEYCDSYGAQTSIKTSATFQSYFKAG 960
Qy	CC	Db	Db 901 PVEPGTIGGAAYQLPAHCLPWCGLULLDTOTLEYCDSYGAQTSIKTSATFQSYFKAG 960	Qy	Qy 961 KTMRNKLLSVTRLKCHGLPFDLQVNLSLQTVICINIVKIFLQAYRFAHCYVQLPPDQRVRK 1020	Db	Db 961 KTMRNKLLSVTRLKCHGLPFDLQVNLSLQTVICINIVKIFLQAYRFAHCYVQLPPDQRVRK 1020	Qy	Qy 961 KTMRNKLLSVTRLKCHGLPFDLQVNLSLQTVICINIVKIFLQAYRFAHCYVQLPPDQRVRK 1020
Db	CC	Db	Db 961 KTMRNKLLSVTRLKCHGLPFDLQVNLSLQTVICINIVKIFLQAYRFAHCYVQLPPDQRVRK 1020	Qy	Qy 1021 NLTFPLGIISSQASCCYATIILKUNQNGMTLKASGSPPPEAHMLCYQAFJLKAHSVYK 1080	Db	Db 1021 NLTFPLGIISSQASCCYATIILKUNQNGMTLKASGSPPPEAHMLCYQAFJLKAHSVYK 1080	Qy	Qy 1021 NLTFPLGIISSQASCCYATIILKUNQNGMTLKASGSPPPEAHMLCYQAFJLKAHSVYK 1080
Qy	CC	Db	Db 1021 NLTFPLGIISSQASCCYATIILKUNQNGMTLKASGSPPPEAHMLCYQAFJLKAHSVYK 1080	Qy	Qy 1081 CLLGFLRTAQKLCKRLPKATMTLKAADPASTDQTILD 1122	Db	Db 1081 CLLGFLRTAQKLCKRLPKATMTLKAADPASTDQTILD 1122	Qy	Qy 1081 CLLGFLRTAQKLCKRLPKATMTLKAADPASTDQTILD 1122
Db	XX	Db	Db 1081 CLLGFLRTAQKLCKRLPKATMTLKAADPASTDQTILD 1122	Qy	Qy 121 SYLPNTVETURVGAMMILLSRGDDLVYLALLAHCALYLLVPPSCAYQVCGSPLYQICA 180	Db	Db 121 SYLPNTVETURVGAMMILLSRGDDLVYLALLAHCALYLLVPPSCAYQVCGSPLYQICA 180	Qy	Qy 121 SYLPNTVETURVGAMMILLSRGDDLVYLALLAHCALYLLVPPSCAYQVCGSPLYQICA 180
Qy	XX	Db	Db 121 SYLPNTVETURVGAMMILLSRGDDLVYLALLAHCALYLLVPPSCAYQVCGSPLYQICA 180	Qy	Qy 181 TTDIWPSVASYRTRPVRGFTNLRPLQQIKKSROEAPKPLAPSRTGKRHLSLTSTS 240	Db	Db 181 TTDIWPSVASYRTRPVRGFTNLRPLQQIKKSROEAPKPLAPSRTGKRHLSLTSTS 240	Qy	Qy 181 TTDIWPSVASYRTRPVRGFTNLRPLQQIKKSROEAPKPLAPSRTGKRHLSLTSTS 240
Db	XX	Db	Db 181 TTDIWPSVASYRTRPVRGFTNLRPLQQIKKSROEAPKPLAPSRTGKRHLSLTSTS 240	Qy	Qy 241 VPSAKKRCRCPYPRVPRGPHQVLPPSGKSWVPSPARSPEVPTAEDLSSKGKVSDLSL 300	Db	Db 241 VPSAKKRCRCPYPRVPRGPHQVLPPSGKSWVPSPARSPEVPTAEDLSSKGKVSDLSL 300	Qy	Qy 241 VPSAKKRCRCPYPRVPRGPHQVLPPSGKSWVPSPARSPEVPTAEDLSSKGKVSDLSL 300
Qy	XX	Db	Db 241 VPSAKKRCRCPYPRVPRGPHQVLPPSGKSWVPSPARSPEVPTAEDLSSKGKVSDLSL 300	Qy	Qy 301 SGSVCCRKHPSTSSTLSPRONAFQRLPIERFLYSPRGQERLNPSFLSNIQPNLT 360	Db	Db 301 SGSVCCRKHPSTSSTLSPRONAFQRLPIERFLYSPRGQERLNPSFLSNIQPNLT 360	Qy	Qy 301 SGSVCCRKHPSTSSTLSPRONAFQRLPIERFLYSPRGQERLNPSFLSNIQPNLT 360
Db	XX	Db	Db 301 SGSVCCRKHPSTSSTLSPRONAFQRLPIERFLYSPRGQERLNPSFLSNIQPNLT 360	Qy	Qy 361 GARRLYEVITIPLGSRPTSGLPCRTHRLSRRYQMRPLFQQLVNHAEQCTYRLJRSHCRP 420	Db	Db 361 GARRLYEVITIPLGSRPTSGLPCRTHRLSRRYQMRPLFQQLVNHAEQCTYRLJRSHCRP 420	Qy	Qy 361 GARRLYEVITIPLGSRPTSGLPCRTHRLSRRYQMRPLFQQLVNHAEQCTYRLJRSHCRP 420
Qy	XX	Db	Db 361 GARRLYEVITIPLGSRPTSGLPCRTHRLSRRYQMRPLFQQLVNHAEQCTYRLJRSHCRP 420	Qy	Qy 421 RTANOOVTDALNTSPPHMDLIRLHSSPPOVYGGPLBACLKVKVSAASLWGTGRHNERFFKVN 480	Db	Db 421 RTANOOVTDALNTSPPHMDLIRLHSSPPOVYGGPLBACLKVKVSAASLWGTGRHNERFFKVN 480	Qy	Qy 421 RTANOOVTDALNTSPPHMDLIRLHSSPPOVYGGPLBACLKVKVSAASLWGTGRHNERFFKVN 480
Db	XX	Db	Db 421 RTANOOVTDALNTSPPHMDLIRLHSSPPOVYGGPLBACLKVKVSAASLWGTGRHNERFFKVN 480	Qy	Qy 481 LKKFISIGKYGKLSQELMWKVKVEDCHWLSSPGKDRPVAEHLRERLATELFWLM 540	Db	Db 481 LKKFISIGKYGKLSQELMWKVKVEDCHWLSSPGKDRPVAEHLRERLATELFWLM 540	Qy	Qy 481 LKKFISIGKYGKLSQELMWKVKVEDCHWLSSPGKDRPVAEHLRERLATELFWLM 540
Qy	XX	Db	Db 481 LKKFISIGKYGKLSQELMWKVKVEDCHWLSSPGKDRPVAEHLRERLATELFWLM 540	Qy	Qy 541 TYVQQLRSRFFYTESTFQQRFLIFFYTKSYWSKLSQSIGVROLERYLRELQSSEVRHQ 600	Db	Db 541 TYVQQLRSRFFYTESTFQQRFLIFFYTKSYWSKLSQSIGVROLERYLRELQSSEVRHQ 600	Qy	Qy 541 TYVQQLRSRFFYTESTFQQRFLIFFYTKSYWSKLSQSIGVROLERYLRELQSSEVRHQ 600
Db	XX	Db	Db 541 TYVQQLRSRFFYTESTFQQRFLIFFYTKSYWSKLSQSIGVROLERYLRELQSSEVRHQ 600	Qy	Qy 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660	Db	Db 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660	Qy	Qy 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660
Qy	XX	Db	Db 601 DTWLAMPICRLRPIKNGLPIRVNMSYSMGTALGRKQAOHTFLRKTFLSMNLYERT 660	Qy	Qy 661 KPHLIMCSVSIGMDITRTRAPFLVRAALQTPRMVFKADTVGAYDA.PQGKLVVEWA 720	Db	Db 661 KPHLIMCSVSIGMDITRTRAPFLVRAALQTPRMVFKADTVGAYDA.PQGKLVVEWA 720	Qy	Qy 661 KPHLIMCSVSIGMDITRTRAPFLVRAALQTPRMVFKADTVGAYDA.PQGKLVVEWA 720
Db	XX	Db	Db 661 KPHLIMCSVSIGMDITRTRAPFLVRAALQTPRMVFKADTVGAYDA.PQGKLVVEWA 720	Qy	Qy 721 NMIRHSESTYCIROVAVRDRSQQGTHSKFSERQVTTLSDLOPMGOFKLHQDSASLR 780	Db	Db 721 NMIRHSESTYCIROVAVRDRSQQGTHSKFSERQVTTLSDLOPMGOFKLHQDSASLR 780	Qy	Qy 721 NMIRHSESTYCIROVAVRDRSQQGTHSKFSERQVTTLSDLOPMGOFKLHQDSASLR 780
Qy	XX	Db	Db 721 NMIRHSESTYCIROVAVRDRSQQGTHSKFSERQVTTLSDLOPMGOFKLHQDSASLR 780	Qy	Qy 781 NSVVIQOSISHNESSSSLEDFPLHLRHSVYKIGDRCYTOCGIPQGSLSLICSLCFG 840	Db	Db 781 NSVVIQOSISHNESSSSLEDFPLHLRHSVYKIGDRCYTOCGIPQGSLSLICSLCFG 840	Qy	Qy 781 NSVVIQOSISHNESSSSLEDFPLHLRHSVYKIGDRCYTOCGIPQGSLSLICSLCFG 840
Db	XX	Db	Db 781 NSVVIQOSISHNESSSSLEDFPLHLRHSVYKIGDRCYTOCGIPQGSLSLICSLCFG 840	Qy	Qy 841 DMENKLPAEVQRDGLLRFVDDFLUTPHDOAKTFLSTLVHGVPYGMCNLQKTVNF 900	Db	Db 841 DMENKLPAEVQRDGLLRFVDDFLUTPHDOAKTFLSTLVHGVPYGMCNLQKTVNF 900	Qy	Qy 841 DMENKLPAEVQRDGLLRFVDDFLUTPHDOAKTFLSTLVHGVPYGMCNLQKTVNF 900
Qy	XX	Db	Db 841 DMENKLPAEVQRDGLLRFVDDFLUTPHDOAKTFLSTLVHGVPYGMCNLQKTVNF 900	Qy	Qy 901 PVEPGTIGGAAYQLPAHCLPWCGLULLDTOTLEYCDSYGAQTSIKTSATFQSYFKAG 960	Db	Db 901 PVEPGTIGGAAYQLPAHCLPWCGLULLDTOTLEYCDSYGAQTSIKTSATFQSYFKAG 960	Qy	Qy 901 PVEPGTIGGAAYQLPAHCLPWCGLULLDTOTLEYCDSYGAQTSIKTSATFQSYFKAG 960
Db	XX	Db	Db 901 PVEPGTIGGAAYQLPAHCLPWCGLULLDTOTLEYCDSYGAQTSIKTSATFQSYFKAG 960	Qy	Qy 961 KTMRNKLLSVTRLKCHGLPFDLQVNLSLQTVICINIVKIFLQAYRFAHCYVQLPPDQRVRK 1020	Db	Db 961 KTMRNKLLSVTRLKCHGLPFDLQVNLSLQTVICINIVKIFLQAYRFAHCYVQLPPDQRVRK 1020	Qy	Qy 961 KTMRNKLLSVTRLKCHGLPFDLQVNLSLQTVICINIVKIFLQAYRFAHCYVQLPPDQRVRK 1020

Db	121	SYLPNTVITETURVSGANMILLSPHMDLRLKCLCRKPEATMILKAADPAULSTDQTILD 1.122	XX	11-JUN-2002 (first entry)
Qy	181	TTDIWPSVASYRPTPVGCRNTNLRLQIKISSRQEAPKELALPSRGTRKHLSTSTS 240	XX	Mouse telomerase protein sequence.
Db	181	TTDIWPSVASYRPTRVGRNTNLRLQIKISSRQEAPKELALPSRGTRKHLSTSTS 240	XX	Mouse; telomerase; promoter; telomerase catalyst subunit; TERT; mTERT; enzyme; transgenic mouse; drug development; anticancer.
Qy	241	VPSAKGARCYPPVREGPYRQLPTPGSKWSPSPARSPEVPTAEDKDLSSKVKVDLSL 300	XX	
Db	241	VPSAKGARCYPPVREGPYRQLPTPGSKWSPSPARSPEVPTAEDKDLSSKVKVDLSL 300	XX	
Qy	301	SGSVCCCKHPSTSIIJSPPRONAFOQPPIETRHELYSRGDGBRLLNFSLLSNLQPNLT 360	XX	
Db	301	SGSVCCCKHPSTSIIJSPPRONAFOQPPIETRHELYSRGDGBRLLNFSLLSNLQPNLT 360	XX	
Qy	361	GARRIVETIIFLGCSRPTSGLCPTHRSLRSTWQMRPLFQOLLYNHAECQYVLLRSHCRP 420	XX	
Db	361	GARRIVETIIFLGCSRPTSGLCPTHRSLRSTWQMRPLFQOLLYNHAECQYVLLRSHCRP 420	XX	
Qy	421	RTANQOVTDAINTSPPHMDLRLHSSPWQYGFPLRACKVUVSASLWGRTRNERRFFKN 480	XX	
Db	421	RTANQOVTDAINTSPPHMDLRLHSSPWQYGFPLRACKVUVSASLWGRTRNERRFFKN 480	XX	
Qy	481	LKKFISLUGKCGKLSQLIMMKVYEDCHWLRSRSGKOPVPAEHLPLERILATEFLWMD 540	XX	
Db	481	LKKFISLUGKCGKLSQLIMMKVYEDCHWLRSRSGKOPVPAEHLPLERILATEFLWMD 540	XX	
Qy	541	TYVQLLRSFVITTESTFQRBLPFKWSVSKLQSIGVQHLLERVLRLSQEVRRHHQ 600	XX	
Db	541	TYVQLLRSFVITTESTFQRBLPFKWSVSKLQSIGVQHLLERVLRLSQEVRRHHQ 600	XX	
Qy	601	DWLAMPICRLRPIPKPENGRLPVINNSYMGTRALGRKQAHTFTQLKTLFSMLNAYERT 660	XX	
Db	601	DWLAMPICRLRPIPKPENGRLPVINNSYMGTRALGRKQAHTFTQLKTLFSMLNAYERT 660	XX	
Qy	661	KPHLNGSSVLMGNDIYRTTAAFTVRYLAJOTPRMVFKAUTGVAYDAIPQKLVVVA 720	XX	
Db	661	KPHLNGSSVLMGNDIYRTTAAFTVRYLAJOTPRMVFKAUTGVAYDAIPQKLVVVA 720	XX	
Qy	721	NMIRSBESTCIRQAVVRDOSQGQTKSFHQVTTISLDPQPMGQFLKHLDSDASLR 780	XX	
Db	721	NMIRSBESTCIRQAVVRDOSQGQTKSFHQVTTISLDPQPMGQFLKHLDSDASLR 780	XX	
Qy	781	NSVVIHQSISSNESSSSLFDFPLHLFLRHSWVKGDRCTYQCGIPOGSSLSTLCSLCFG 840	XX	
Db	781	NSVVIHQSISSNESSSSLFDFPLHLFLRHSWVKGDRCTYQCGIPOGSSLSTLCSLCFG 840	XX	
Qy	841	DMENKLFAEVQPDGLLIREPDDFLPLAQKTFSLTLYHGVPEYGMINLQKTUNF 900	XX	
Db	841	DMENKLFAEVQPDGLLIREPDDFLPLAQKTFSLTLYHGVPEYGMINLQKTUNF 900	XX	
Qy	901	PVEPGTGGAAFYQLPAHCFLFWCGLUDTQLEFCDYSGYAQTSLKTSLIPQSVPKAG 960	XX	
Db	901	PVEPGTGGAAFYQLPAHCFLFWCGLUDTQLEFCDYSGYAQTSLKTSLIPQSVPKAG 960	XX	
Qy	961	KTMRNKLLSVRLKCHGLFDLQVNSLQTVCIINYKIFLQOYRFHACVIQLPFDQVRK 1020	XX	
Db	961	KTMRNKLLSVRLKCHGLFDLQVNSLQTVCIINYKIFLQOYRFHACVIQLPFDQVRK 1020	XX	
Qy	1021	NLTFFGLGISSOASCCYAIJKKPNPCTLJKASSGSPPPBAHPLCYQAFLKLAAHSVYK 1080	XX	
Db	1021	NLTFFGLGISSOASCCYAIJKKPNPCTLJKASSGSPPPBAHPLCYQAFLKLAAHSVYK 1080	XX	
Qy	1081	CLLGPartQAKLCLCRKPEATMILKAADPAULSTDQTILD 1.122	XX	
Db	1081	CLLGPartQAKLCLCRKPEATMILKAADPAULSTDQTILD 1.122	XX	
Qy	301	SGSVCKHPKSSTSISLSPPRONAFOQLRPFTETRHFYLSRGQGQERINPSLLSNQPNLT 360	XX	
Db	301	SGSVCKHPKSSTSISLSPPRONAFOQLRPFTETRHFYLSRGQGQERINPSLLSNQPNLT 360	XX	
Qy	361	GARRIVETIIFLGSRPTSGPLCIRTHRLSRYWMPFLFOQVLYNHABCQYVRLRSHCRF 420	XX	
Db	361	GARRIVETIIFLGSRPTSGPLCIRTHRLSRYWMPFLFOQVLYNHABCQYVRLRSHCRF 420	XX	
Qy	421	RTANGQVTDALNTSSPHMDLRLKCLCRKPEATMILKAADPAULSTDQTILD 1.122	XX	
Db	421	RTANGQVTDALNTSSPHMDLRLKCLCRKPEATMILKAADPAULSTDQTILD 1.122	XX	

PI	Majumdar A,	Ferber IA,	Frolkis M,	Wang Z;
XX	XX	XX	XX	XX
WPI;	2004-071946/07.			
Db	421 RTANQQTVDALATSPPHMDJRLHSSPWOYGFRLACLKVKVASILWGTNHNEHRFFCN	480		
Qy	481 LKKPISLGKYGKSLQBLMWKVKVEDCHWLRSSPGDRPAEHRERLATEFLWMD	540		
Db	481 LKKPISLGKYGKSLQBLMWKVKVEDCHWLRSSPGDRPAEHRERLATEFLWMD	540		
Qy	541 TIVVQLRSPFTESTQKLRLFFYTKYSVNSKLSQSTGVROHLERYRLRELSEQEYRHQ	600		
Db	541 TIVVQLRSPFTESTQKLRLFFYTKYSVNSKLSQSTGVROHLERYRLRELSEQEYRHQ	600		
Qy	601 DTWAMPICRIPKPGNLRTIVMSYSMGTRALGRKQHQHTFKLTKLFSMLNERT	660		
Db	601 DTWAMPICRIPKPGNLRTIVMSYSMGTRALGRKQHQHTFKLTKLFSMLNERT	660		
Qy	661 KHPHMGESVLGNNDITYTWRFLRVALDPTPRMFTVADTVGAYDAFPQKLIVEVA	720		
Db	661 KHPHMGESVLGNNDITYTWRFLRVALDPTPRMFTVADTVGAYDAFPQKLIVEVA	720		
Qy	721 NMTRHSBETYCTROYAVVRDSDQGVHSKSFRRQVTTLSDLOPQMGLKHLQDSASLR	780		
Db	721 NMTRHSBETYCTROYAVVRDSDQGVHSKSFRRQVTTLSDLOPQMGLKHLQDSASLR	780		
Qy	781 NSVIEQSISNESSSEDFELTHLBSVVKIGDACTQCGIIPQOSLSTLCSLCFG	840		
Db	781 NSVIEQSISNESSSEDFELTHLBSVVKIGDCTQCGIIPQOSLSTLCSLCFG	840		
Qy	841 DMENKLPFAEVQFDGLLRFVDDFLLYTPHLDQAKTFLSTLVHGVPBYGMCMNLQKTVVNF	900		
Db	841 DMENKLPFAEVQFDGLLRFVDDFLLYTPHLDQAKTFLSTLVHGVPBYGMCMNLQKTVVNF	900		
Qy	901 PVEPGTLLGAAAPYQOLPAHCLFWPGGLLIDDTOTLEFDYSGAQTSIKTSITFQSVFKAG	960		
Db	901 PVEPGTLLGAAAPYQOLPAHCLFWPGGLLIDDTOTLEFDYSGAQTSIKTSITFQSVFKAG	960		
Qy	961 KTMNRKLLSIVDLRKCHGFLDQVNSLQTCVNCNIYKPLQAYRFLACVILPFDQRVK	1020		
Db	961 KTMNRKLLSIVDLRKCHGFLDQVNSLQTCVNCNIYKPLQAYRFLACVILPFDQRVK	1020		
Qy	1021 NTFPFLGISSQASCYIALKYVNPENTLKAAGSGSFPEEAHLWLYCQFLKLAHAHSVYIK	1080		
Db	1021 NTFPFLGISSQASCYIALKYVNPENTLKAAGSGSFPEEAHLWLYCQFLKLAHAHSVYIK	1080		
Qy	1081 CIGGPLRATAQKLICRKLFPEATMTILKAADPALSTDQFTILD	1122		
Db	1081 CIGGPLRATAQKLICRKLFPEATMTILKAADPALSTDQFTILD	1122		
RESULT 4	ADG90609	standard; protein; 1152 AA.		
ID	ADG90609	standard; protein; 1152 AA.		
XX	XX			
DB	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	459		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
DB	420 SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	479		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	495		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	398 LSLSGSVCCXHKPS-TSLSSPRONAQLRP-FLETPLHLYSPPARSPVEP--TAEKDLSSKGKVSD	297		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	355		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	421 VPSAKKARYCVPVRYTEGPHRQVLTPSGKSWPSPARSPVEP--TAEKDLSSKGKVSD	297		
Db	241 LPLPKCARRGAAPBZERTPVGQGSMPGKPNPTNGCPRAWNNSVREACVPLGPSPGAKBRGGSASRS	240		
Qy	298 LSLSGSVCCXHKPS-TSLSSPRONAQLRP-FLETPLHLYSPPARSPVEP--TAEKDLSSKGKVSD	355		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	420 SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	479		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	456 RACLCKVKSAASLGWTRHNERPFLQKLFSLGKGLKSLQELMKMKVQEDCHAWRSPG	515		
Db	480 RACLCKVKPGLGGSRHNERFLKVNKKFISLGKHLKSLQELTMKVRDCANWRSPG	539		
Qy	516 KDRVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	572		
Db	540 YESVPAEHRERLRLA--TFLWLMDTVVQLLRSPPFTTESTQKRNLLFFYKRSVWS	599		
XX	XX			
DT	SHCPRAAATPVAGALNTSPQQGSVAPEVVAAPBQTDSTRMLQRHSSPGLVRLRRSPG	455		
DB	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	419		
Qy	416 SHCRPTANQVTTDALNTSPP-----HLMQMLRLHSSPQYGYGL	455		
Db	301 LSLSGSVCCXHKPS-SPPLSSPPRONAQLRPVZAEKPLQVLLVNAECQYVRLR	359		
Qy	356 QPNLTGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR	415		
Db	360 QPSLIGARRLVEETIPLGSRWTSGLCRTRFLSRVWQPLFQELIGHARCPYRLRR</td			

Db 660 RAGGRRIKQAHFTORLKLTLFSVLYERTKPHILGASVLGMNDIYRTWTFVLRVRLALDP 719
 Qy 693 TPNMFYRADVTGAYDAIPQGLKVEVANMTRHSESTYCIROYAVYVRRDSQGVHKSFR 752
 Db 720 TERMFYRADVTGAYDAIPQDLKVEVANMTRHSESTYCIROYAVYVRRDSQGVHKSFR 779
 Db 753 QVTTLSIDQIOPMQFLKLQDSASALRNSVIEQTSIMNNESSSSLFDFFLFLHLRSVVK 812
 Qy 780 QVTTLSIDQIOPMQFLKLQDSASALRNSVIEQTSIMNNESSSSLFDFFLFLHLRSVVK 839
 Db 813 1GDRCYTCQCGIPQGSSTLICSLCQDMENKLFAEVQRDGLLRFVDDFLFLVTPHLQD 872
 Qy 840 1GCRCYTCQCGIPQGSSTLICSLCQDMENKLFAEVQRDGLLRFVDDFLFLVTPHLQD 899
 Qy 873 AKTFLSTIVRGGT/PBYGMNINLQTKTVWAFFPVEGSTLGAAPIYOLPAHCFPMCGLLUDQT 932
 Db 900 AKTFLSTIVRGGT/PBYGMNINLQTKTVNPVEGSTLGAAPIYOLPAHCFPMCGLLUDQT 959
 Qy 933 LEVFCDYSGYAOTSISIKSTLTOSVFKAGKTMWNKLISVSLRKCHGLFLDQVNSLQTCI 992
 Db 960 LEVFCDYSGYAOTSISAKSLTFTQVFKAGKMNKLJSVSLRKCHSLFDLQVNSLQTCI 1019
 Qy 993 NYKIFLQAYRPHACVQLPPDQRVKNLTFPLGTSQSACCCYAIKYKVRNPKGHTLK-- 1050
 Db 1020 NYKIFLQAYRPHACVQLPPDQRVKNPFTPLGTSQSACCCYAIKYKVRNPKGHTLK 1079
 Qy 1051 -AGSPPPEAIAWLCYAFALLKLAANSVITYCKLGPARTAQKLLCRKLPRATMILLKAAA 1109
 Db 1080 GRAGSPFPEARAWLCYAFALLKLAANSVITYCKLGPARTAQKQLCRKLPRATMITLEAAA 1139
 Qy 1110 DPAALSTDFQTILD 1122
 Db 1140 DPAALSTDFQTILD 1152
RESULT 5
 ADD21416 standard; protein; 1128 AA.
 XX ADD21416;
 XX DT 15-JAN-2004 (first entry)
 DE Golden hamster TERT protein related to continual cell growth.
 XX continual growth; cultured cell; cyclin dependent kinase; cdk4; cdk2;
 KW cdk6; activating mutation; cell growth; cell division; cell cycle;
 KW cancer-causing agent; continual growth-induced cell; enzyme; TERT;
 KW telomerase; Golden hamster.
 XX Mesocricetus auratus.
 XX PN WO2003044169-A2.
 PD 30-MAY-2003.
 XX PP 15-NOV-2002; 2002WO-US036729.
 PR 15-NOV-2001; 2001US-0334760P.
 XX (UTEM) UNIV TEMPLE.
 PI Reddy PE, Rane SG, Mettus RV;
 XX DR WPI: 2003-449813/42.
 XX A composition for reversibly inducing continual growth in normal cells;
 PT comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or
 PT its active fragment, derivative, homolog or analog, having an activating
 PT mutation.
 XX Disclosure; Page 119-121; 7pp; English.
 PS PS

CC This invention relates to a novel composition for inducing a reversible
 CC state of a continual growth in cultured cells and comprises at least one
 CC compound comprising a cyclin dependent kinase (cdk4, cdk2 or cdk6
 CC protein having an activating mutation. Growth and division of living
 CC cells involve a regular series of events and processes that comprise the
 CC cell cycle. Cyclin dependent kinases cdk2, cdk4 and cdk6 are involved in
 CC the control of G1, the point at which cells irreversibly commit to DNA
 CC synthesis and thus enter the cell cycle. The invention is useful in
 CC reversibly inducing continual growth in normal cells and may allow the
 CC screening of cancer causing agents with the continual growth-induced
 CC cells. The present sequence is that of the golden hamster TERT protein,
 CC the catalytic subunit of telomerase, related to the invention. Note: Due
 CC to an error in the specification or sequence listing, the Seq ID numbers
 CC given in the disclosure do not correspond to those given in the sequence
 CC listing. It is therefore unclear which Seq ID number corresponds to which
 CC sequence and exactly which sequence is being claimed.
 XX
 Sequence 1128 AA:
 SQ Query Match 80.5%; Score 4751; DB 7; Length 1128;
 Best Local Similarity 80.4%; Pred. No. 0;
 Matches 904; Mismatches 127; Indels 8; Gaps 4;
 保守性 90; 保守性 90; Mismatches 127; Indels 8; Gaps 4;
 Matches 904; 保守性 90; Mismatches 127; Indels 8; Gaps 4;
 Qy 1 MTRAPCPAVRSLLRSRYRWPLATFVRLGSPGRLLYQGDPLKLYTVAQCLYCMHW 60
 Db 1 MPRAPCRATVALLRSQYRQWPLATFVRLGSPGRQVGDPLKVRVRLTVALRCYCVPW 60
 Qy 61 GSQQPPADLSPHQVSQSLKELVARYVORLCERNERNVLAFLGPFELLTEARGGPPMFTSSVR 120
 Db 61 DSQQPPADLSPHQVSQSLKELVARYVORLCERGVRNLTFGALLNCAGQGPMPMTFTSSVR 120
 121 SYLPNTVITLRSQAWMILLSRVGDLLVYLALLCALYLVPPSCAYQVGSPSPYQICA 180
 Db 121 SYLPNTVITLRSQAWMILLSRVGDLLVYLALLCALYLVPPSCAYQVGSPSPYQICA 180
 Qy 181 TTDIIVSVASYRPRPGVANPTNIRFLQQTQKSSRQEAKPLAPLSPGRTGKHLISLTSTS 240
 Db 181 TAETWPSVSR1YRFPVGFMNTHLGSTHRVRNSSHQEWAKKPPLPSBREAKRSLSITNRS 240
 Qy 241 VPSACKARYCVPVREBGPQVQLPPGSPGSWVPSPARSPEV--TAKDOLSSKCVSD 297
 Db 241 VPPSGKARCIDLAPRKGPTRQAVTPPSDKTWVPPAKSHAVPISRTKEDLSSGKAPG 300
 Qy 298 LSLSGSVCCTKHKPSTSLSSPRONAQFLQRPFIETTRHFLYSRGDGQERLNSFLSNLQP 357
 Db 301 LSRSGIVCYRHKPSSTSLSQPLCQAFQURPFTPSDTKWTWVPPAKSHAVPISRTKEDLSSGKAPG 360
 Qy 358 NLTGARRLVEITPLSRSRPRSGPLCQFLTRHLSRYYQMRPLPQOLYHARQCYTFLRSH 417
 Db 361 SUTGARRLVEITPLGMRPRFGSPLOGRRLSKRYVQMRPLFQQLJVNHARCPYVRLRSH 420
 Qy 418 CRFRTANQQTDDALN-TSPPHLMQDGLRLHESPWQYGFLEACLCKVVSASWNGTHEINERR 476
 Db 421 CRFRTAHQVAGALTTSPOBLMLNLRLLHSPWQYGFLOACVGCLVPPGIGWGRHNQRR 480
 Qy 477 FFPTNKKPISIGKYGKSLSIQBLMMYKVEICHWLSRSPGKDRVPAAEHRLLRERLTLATELP 536
 Db 481 FFKNYTRPISIGKYGKDLISQBLTMKQVDCRMWISSPGNCVPAEHRTRERLTLAVFLP 540
 Qy 537 WLMDTIVQQLRSRSPFYTTESTFQKRLPFTRKSVSKLQSGTIGVRLERYLRESQBEV 596
 Db 541 WLMDAVVELRSRSPFYTETTFQKRLPFTRKSMRRLQSGVRLERYLRESQBEV 600
 Qy 597 RHHQDTWLAMPICRIPFIPKPGNGLPEVINSYSMTRALGRKQOHFTORLKTFSMLN 656
 Db 601 QRQRQAWPAMPICRIPFIPKPGNGLPEVINSYSMTRALGRKQOHFTORLKTFSMLN 659
 Qy 657 YERTKPHFLMGSSVGLMNDIYRTMRAFYLVRALDQTPRMYFVYKADTGYDAYATPGKLV 716
 Db 660 YBLTGHTNLIGASVGLNDIYRTMWFVLRVRLTLPAPRMFMVKCDVGTAYDAYATPGKLV 719
 Qy 717 EVVANNIRHSESTYCRQYAVVRRDSQGVQHKSFRRQVTTLSQDPMGOFLKHKHQDSDA 776
 XX

Db	720	EVIAMIRHPDPSYCITHQYAVVQRDRQQTHKSFRQVSTLSDLOPHMMGOFKLHQDSST 779	xx	Sequence 1128 AA;
Qy	777	SALRNSVTEQISNESSSLEDFPFLHPLHSNTVKIGBCYTQCGIPOGSSLSTLCS 836	SQ	Query Match 80.5%; Score 4751; DB 8; Length 1128;
Db	780	SALRNSVTEQISNESSSLFDPFLRVSNTVKIGRCYVQCGIPQGSSSLTLCs 839	Best Local Similarity 80.1%; Pred. No. 0;	
Db	837	LCFGDMENKLPAEVQDGLLRFVDDPLVPHDOAKPLFLSTLVHGVPIYGCMINLQTT 896	Matches 904; Conservative 90; Mismatches 127; Indels 8; Gaps 4;	
Qy	840	LCFGDMENKLPAEVQDGLLRFVDDPLVPHDOAKPLFLSTLVHGVPIYGCMINLQTT 899	Qy	1 MTRAPRCPAVSLRSRTRYWPLATPVRLLGPGRRLVQPGDPKIVRTLVAQLVCMEW 60
Db	897	VNFNPVBPGLGGAAPIYQLPAHCLPFWCGMILDTOTLEVCDYSGYAOTSIKTSLTFQSV 956	Db	1 MPRAPCRAYRALRSIQTRQWPLATPVRLLGPGRRLVQPGDPKIVRTLVAQLVCWV 60
Qy	900	VNFNPVDAQTLDGTAGLPQAHCLPFWCGMILDTOTLEVCDYSGYAOTSIKTSLTFQTT 959	Qy	61 GSQPPADLSFHQSISLKELVARVYORLCERNERNVNLAFGFBLINEARCGPMAFTSSYR 120
Db	957	FKAGKTMKVLKLSLBKCHCFLDOLQNSLQTCINTYKIELQAYRTHACVQLPFDQ 1016	Db	61 DSQPPADLSFHQSISLKELVARVYORLCERNERNVNLAFGFBLINEARCGPMAFTSSYR 120
Qy	960	FKAGKRMRMKQXKLLAVLRLKCHSISLQTMNSLQTCINTYKIELQAYRTHACVQLPFDQ 1019	Qy	121 SYLNPNTVIETLRYSGAAMILLSRNGDDLYLLAHCALYLVPPSCAYQVGSPLYQICAA 180
Db	1017	RVRKNUTPFLGISSOASCCYAILKVKRNPTLKK--ASSSFPPAAHHWYCQAPLKA 1073	Db	121 SYLNPNTVIETLRYSGAAMILLSRNGDDLYLLAHCALYLVPPSCAYQVGSPLYQICAA 180
Qy	1020	HVRKNDPAPLSSITNTASCCYISLCKRNAMTILRKGAASSPPEARWYCQAPLKA 1079	Qy	181 TTDIWPSPVASYRPTRPVGRNPNFLRLQPKSSRQEAKPLALPSRGTKRHJLSLTSTS 240
Db	1074	AHSVLYTKCLLGSPLRTAQKLLCRLKPEATTWTLKAADPDLSTDPTQTLID 1122	Db	181 TAETWPSPVSIYTRTPVGRNFTLGSITVRVSSHQEWKPPLPSREAKRSLISITRS 240
Qy	1080	GHSVTYTKCLLGSPLRTAQKQLCRLKPRATMATELAADPDLSTDPTQTLID 1128	Qy	241 VPSAKKARCYCPVPVTEEGPHROVLPTPSGSKMSWPSPARSPPEVP--TAEKDQLSKKGKVSD 297
Db	RESULT 6		Db	241 VPSAKKARCDLAPRKEQGPyRQAVTPPSDXTQWNPAPKSHAVP1SRTKBDLSSGVKAEG 300
ADG90603	1D	ADG90603 standard; protein; 1128 AA.	Qy	298 LSLSGSVCCKHKPSSTSLSPPRONAFQLRPFETRHPLYSRGDGQERLNPSFLSNLQP 357
XX	25-MAR-2004	(first entry)	Db	301 LSRSGSVCYKHKPSSTSLSPLCQNAFQLRPFETKRLPYSREGGRERLNPSFLNLQP 360
XX	Hamster TERT SEQ ID NO:6.		Qy	358 NLTGARRLIVB1IFG5RSPRTISPLCRLTHRLSRRYWMQMLPFOQLVNHAECQVRLLRSH 417
XX	hamster; immune response; telomerase reverse transcriptase; TERT; cytotoxic; immunostimulant; cancer; cytotoxic T cell response.		Db	361 SLTGARRLIVB1IFG5RSPRTISPLCRLTHRLSRRYWMQMLPFOQLVNHAECQVRLLRSH 420
XX	cytotoxic; immune response; telomerase reverse transcriptase; TERT; cancer; cytotoxic T cell response.		Qy	418 CRPRTANQOVTDAIN-TSPPHLMMDLRLHSSPMQVYGLPRLACIICKVVSASLWGTNRNBR 476
XX	Mesocricetus auratus.		Db	421 CRPRTAAHOVAGAALNTTSQRLMLRLHSSPMQVYGLPQLACVSKLVPPEGLWSBRHNQRR 480
OS			Qy	477 FPKNQKKEFISLGKYGKLSQLQELMKMKDVECHNTRSSPSKDRYPAEHLRERLIAFLP 536
DT			Db	481 FFKQVTKRFISLGKDYKLSQLQELTMKWDCRMTRSSPNCPNYPAEHTTRERLAVFLP 540
DE			Qy	537 WLMDTYVWOLLSPFVTESTFKQNLFPYKSYWSKLQSIGYRQHLERVRLSLSQEVY 596
XX			Db	541 WLMDTYVWOLLSPFVTESTFKQNLFPYKSYWSKLQSIGYRQHLERVRLSLSQEVY 600
XX			Qy	597 RHHQOPTWLAMPICRURFIPKPGNGLRPIVNMYSNGTRALGRKCOQHFTQRLTKLFSMLN 656
PN	WO2004002408-A2.		Db	601 QRQQAWPAMPICRURFIPKPSGURFIPVNMYS-MGTRAEDFKGKOQHFTQCLTKLFSVLN 659
XX			Qy	657 YERKTHPHMGSSVILGMNDIYRTWRAFYLRVRLADQTPMVFYKADVTCAYDA1PQGKLV 716
PD	08-JAN-2004.		Db	660 YELTKHTNLIGASVTLGNDIYRTWTRTFVLRVRLDAPAPMYFVYKADVTCAYDA1PQDQLV 719
XX	WPI: 2004-071946/07.		Qy	717 EVVANNMRHSESTVCIQYAVVRRDSQGQVHKSPRQVTTLSDLQPYNCQFLKHQLQSDA 776
XX	N-PSDB: ADG90602.		Db	720 EVIAMIRIPDNSTICHQYAVVQRDRQGOTHKSTRQVSTLSDLQPHMCOFLKHQLQSDP 779
XX	Biliciting an immune response in a mammal specific for its own telomerase reverse transcriptase (TERT), useful for treating or preventing cancer, comprises administering a protein with at least 20 consecutive amino acids of TERT of another mammalian species, or a nucleic acid encoding the protein. A composition of the invention has cytotoxic, and immunostimulant activity. The protein or the nucleic acid encoding the protein is useful in the manufacture of a medicament for the treatment of cancer in a human or for eliciting a cytotoxic T cell response in a human.		Qy	777 SALRNSVTEQISMNNESSSSLFDFFLHPLRHSVTKIGDRCTYQGTPQGSSLSTLCLS 836
PR	27-JUN-2003; 2003WO-US019844.		Db	780 SALRNSVTEQISLINESSSLFDFFLPVRNSVTKIGRCYVQGIPQGSSLSTLCLS 839
XX	PR 27-JUN-2002; 2002US-0393295P.		Qy	837 LCFGMENKLFAEVQDGLLRFYDDEFLYTPHLDQAKTFLSTLWVGPBYGCMTNLQKT 896
PA	(GERO-) GERON CORP.		Db	840 LCFGMENKLFAEVQDGLLRFYDDEFLYTPHLDQAKTFLSTLWVGPBYGCMTNLQKT 899
XX	Majundar A, Ferber IA, Frolikis M, Wang Z;		Qy	897 VNNPFPVPEPTLGGAPQQLPAHCLPWCGLLIDDTQTLVPCDYSQATSIKTSUTPQSV 956
XX	WPI: 2004-071946/07.		Db	900 VNNPFPVDAITLDGTPAAPHOLPAHCLPWCGLLIDDTQTLVPCDYSQATSIKTSUTPQSV 1016
DR			Qy	957 PKAGKTMKVLKLSLBKCHCFLDOLQNSLQTCINTYKIELQAYRPHACTVQLPPDQ 1016

Db 950 FKGAGRNMRQKLLAVIRLKHSLFLDLQNSLQTYCINTVYKIFLQAYRFRHACALQLPFDQ 1019
 Qy 1017 RVRKNLTFFGIGIISQASCCYATLKVKNPGMTLK---ASGSFPEAAHWLYCYOAFLKLKA 1073
 Db 1020 HVRKNPAPLTSISNIASSCCYTLKVKAGMTLKAKGSGSFPPEARWLQYOAFLKLKA 1079
 Qy 1074 AHSVTKYCKLGLPLRTAQKULCRKLPEAMTILKAAADPALSTDFTQTLID 1122
 Db 1080 GHSTYTKCILGLPLRTAQKOLCRKLPEAMTILKAAADPALSTDFTQTLID 1128

RESULT 7
 ID AAW46957 standard; protein; 1132 AA.
 XX
 AC AAW46957;
 XX 13-AUG-1998 (first entry)
 XX Human telomerase reverse transcriptase.
 XX Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
 KW cell proliferation; cancer; ageing; ribonucleoprotein.
 XX OS Homo sapiens.
 PN GB231791-A.
 XX PD 08-APR-1998.
 XX PP 01-OCT-1997; 97GB-00020890.
 PR 01-OCT-1996; 96US-00724633.
 PR 18-APR-1997; 97US-00844419.
 PR 06-MAY-1997; 97US-00846017.
 PR 09-MAY-1997; 97US-00851843.
 PR 14-AUG-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00915503.
 PA (GERON CORP.
 PA (UYTE-) UNTV TECHNOLOGY CORP.
 PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 XX WPI: 1998-171633-16.
 DR N-PSDB, AAV22379.

Pt Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.

PS Claim 3: Fig 17; 387pp; English.

XX The present sequence represents human telomerase reverse transcriptase (hTRT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase RNA component; (C) detection of the hTRT or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions

CC that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods
 XX
 SQ Sequence 1132 AA;

Query	Match	59.4%	Score 3505;	DB 2;	Length 1132;
	Best Local Similarity	62.4%	Pred. No. 0;		
	Matches 719; Conservative	122;	Missmatches	260;	Indels 52;
					Gaps 13;

Qy 1 MTRAPRCRPAVSLRSIISREYRMLPLATVRRRLGPEGRRLVQEDPKYRTLVAQCLIVCMW 60
 Db 1 MTRAPRCRPAVSLRSIISREYRMLPLATVRRRLGPEGRRLVQEDPKYRTLVAQCLIVCMW 60
 Qy 61 GSQPDPADLSFHQVSSILKELYARVWRBLCEARNENVLAQFPELINEARGPPMPTSSVR 120
 Db 61 DARPPPAAPSFHQVSCILKELYARVWRBLCEARNENVLAQFPELINEARGPPMPTSSVR 120
 Qy 61 SYLNPNTVIEITLRVSGIAWMLLSRGVDLLVYLARCALYLLVPPSCAYQVCSPLYQICA 180
 Db 121 SYLNPNTVTDALKSGAWGILLLRVGDVLVHLARCALFVLYVAPSCAYQVCSPLYQICA 180
 Qy 181 TDIDIWPSVSASYTRPTEPVGRNFTNLNRLQQIKSSRQEQAAPLAPSRSRGTRHSLSTSTS 240
 Db 181 ATQRAPPHAS GPRRLQG-----CERAWNHYSTREAGYPLGLPAGAERRGGGASRS 231
 Qy 241 VPSAKKARCYPPVREEGP-----HRQVLPLTPSKSW-VPSPARSPVPTAERDLSK 292
 Db 232 LPLPKPFRRGAAPEPRTPVCGSWAHPGTRGPSPDRGFCVYSPAR-----PAEATSL 286
 Qy 293 GRVSDLSLSS-GSVCKRKHKPSSTSLLSPRONAFQLRP-FIETRHFLYSRGDPQERINPSPF 350
 Db 287 GALSGTHSHSHPSVGROHAGPPSTSRRPRPDTPCPVVAETKHFYLISSGD-KBQLRPSF 345
 Qy 351 LLSNLQPNLTGARRLVEIIPGSRPTSGPLCRTHLSRSRYWQMPFLFQQLVNNHACQY 410
 Db 346 LISSRPSLITGARRLVEIIPGSRPMGTPRRLPRLPQRTWQMPFLPLELGNHACQPY 405
 Qy 411 VRLLRSHCRCPTANQVTDAL-----NTSPPHMMDLRLHSPWQVY 452
 Db 406 GVLKLTKCPLRAA--VTPAAGVCAKEKPQCSVAPEEEDTDPRLVQJLRQHSPPQVY 462
 Qy 453 GFLRACIICKVSYASLNGTRINERRFKNLKCPKISLGKYGKLSLQELNMWKNUVBDCHWLRS 512
 Db 463 GFVRAICURRLVPPGLMSRNRFLNTRKPKISLQELTWKNSVRDCAWLRR 522
 Qy 513 SPGKDQVPAABHLRERILATEFLFVMDTYYVQLRSFYTTESTFQKNLUFFYKRSVWS 572
 Db 523 SPGVGCVPAABHLRERILAKPLWHTMSVTVBLRSFYTETEFQKNLUFFYKRSVWS 582
 Qy 573 KLSQISGYQHQLERVRLRELSEBEVHHQDTWLAMPICRLPKPKNGLRLPVMMSYSMG 632
 Db 583 KLQSISGYQHQLERVRLRELSEBEVHHQDTWLAMPICRLPKPKNGLRLPVMMSYSMG 642
 Qy 633 RALGREKQAOAHTFQRLKTLFSMNLNVERTKPHLMGSVLGANDYTRTWRFLVRLRALDQ 692
 Db 643 RTFRERKERAERLTSVKAFLSVLNTERARRPGLLGA5VGLDDIRHAWRTFVLRAQDP 702
 Qy 693 TPRMYTVKADYGTGADTAIPQSKLVEVYANMTRHSESTYCYROYAVYRVRDSCQVKSFR 752
 Db 703 PPELFYVQVNDTGATDTPDRLTVTASTIK-PONTYCYRRAVYQKAAHGHVYKAFKS 761
 Qy 753 QVTTLSDLQPMGQFLKHLQDSASALRNSWVIESISMNESSLFDFFLHFLRHSVVK 812
 Db 762 HVSTLTDLQPMGQFLKHLQDSASALRNSWVIESISMNESSLFDFFLHFLRHSVVK 819
 Qy 813 IGDRCTYCTOCGIPQSSLSTLCLSFGDMENKLPAEVQDGLLURFVDDFLYVTPHLDQ 872
 Db 820 IRGKSYVQCGIPQSSLSTLCLSFGDMENKLPAEVQDGLLURFVDDFLYVTPHLDQ 879
 Qy 873 AKTFPLSTLVRGVPETGCMINLQKTVUNPFYBPGTIGGRARYQLPPHCLFPWCGJLUDTQT 932
 Db 880 AKTFPLSTLVRGVPETGCMINLQKTVUNPFYBPGTIGGRARYQLPPHCLFPWCGJLUDTQT 939

		SQ	Sequence 1132 AA:
Qy	933 LEVFCDYSGYAQTTSIKTSLTQSVPKAGITMRKLLSVRLKCHGLFLDQVNSLQTYCI 992	Query Match	59.4% ; Score 3505; DB 2; Length 1132;
Db	940 LEVQSDYSIARTSRAISLTPNQGRKAGAMMRKLFGVURKCSLPLDQVNSLQTYCI 999	Best Local Similarity	62.4%; Pred. No. 0;
Qy	993 NIYKIPLLQAYRFHACVOLPFDQYRKNLTFFLGISSOASCCYALLKVKNPENTLKS 1052	Matches	122; Mismatches 719; Conservative 122;
Db	1000 NIYKILQAYRFHACVOLPFDQYRKNLTFFLGISSOASCCYALLKVKNPENTLKS 1059	Qy	1 MTRAPRCPAVRSILRSRYSREWPLATFYRRLGPEGRRLYQPGDPKIVRTLYAQCIVCMHW 60
Qy	1053 GS---FPPPEAHWILCQAFELKLAHSVTKCLGPIPAQKLLCRKLDEATMILKA 1109	Db	1 MTRAPRCPAVRSILRSRYSREWPLATFYRRLGPEGRRLYQPGDPKIVRTLYAQCIVCMHW 60
Db	1060 GAAGPLPSAVQWLQHAFULKLTHRVTTVPLLSRLTAQTLRSRKLCPTTLEAAKA 1119	Qy	61 GSQPBDLFSHOVSISLKELVARYVQLCERNERNVLAFGFELLVQRLGPWLRQVRGPDAFAFLVAQCLVCYRN 60
Qy	1110 DPALSTDFFQTILD 1122	Db	61 DARPAAFSFQVQSCLEKELVARYQLCERGAKVNLAVLGPAFFTTSYR 120
Db	1120 NPALPSDFRTILD 1132	Qy	121 SYLPNTVIELTRVSGAWMILLSRVGDLLVYLLAHCALYLVYLLVPPSCAYOVCGSPLYQICA 180
		Db	121 SYLPNTVTDALRGSGAWGILLRQGVDDVLVHLARCALEFLVLFVASCAQVCGSPLYQICA 180
		Qy	181 TTDIWPSSVASYRPTRPVGRNFTNLRFLQQIKSSRSQEAQPKLALPSPRTKHLSTSTS 240
		Db	181 ATQARPPHEAS-GPRBRIG-----CERAWNHSVREAGVPGICLPAPEARRGGSAAKS 231
		Qy	241 VPSARKARCYPVPRVEBGP-----HHQVLPLTPSGKSM-VPSPARSPEVPTAEKDLSKK 292
		Db	232 LPLERKRPRGAAPEPERPVPGQGSWAHPGCRTRGPDSRFGCVWSPAR----PAEATSLUE 286
		Qy	293 GKVDLSLS-GSYCCXHKPSSTSLLSPRONAFOLRP-FIETRHFLYSLRGDGOERLNPSF 350
		Db	287 GALGSTRHSHPSVGRQHAGPPSTSRRPPWDTPCPYPAETKHFLYSGD-KEQLRSP 345
		Qy	351 LLSNLQPNITGARLVEIIFLGSRPTSGPLCKTRHLSRRYQMRPLFQQLVYNAECOY 410
		Db	346 LLSSSRPSTTGARLVEITFLGSRPWPMPCTPRLPLPRLPQYRPLPBLGHAQCPY 405
		Qy	411 VRLJLISHCFCRTANQVTDAL-----NTSPHMLMDLRLHSSPKQYV 452
		Db	406 GVLLKTHCPLRAA--VTPAAGYCAREKPKQGSVAAPEEBDTDPRLVQLLROISSSPWQYV 462
		Qy	453 GFLRACLCKVVSASLWGTRHNERPFRFKNLUKKPISLGKYGKSLSQBLMWYRMKVECHWLR 512
		Db	463 GFVZACLRLLVPPSLWGSHNERPFLRNTKCFISLGKHNLSQBLTWMSVRDCAWLRR 522
		Qy	513 SPGKDVRPAAEHRLRERILATEFLWLMDTYYVQLRSPPYITESTFOKNRLFPYRKSWS 572
		Db	523 SPGVCVPAAEHRLRERILATEFLWLMDTYYVQLRSPPYVETTFQKNRLFPYRKSWS 582
		Qy	573 KLGISTGVRohleryvrlrelsQEEVRRHQDWTWAMPICLRLPKPKNGLRPIVNMYSMGT 632
		Db	583 KLQSGTIRQHKLKVQLRSELSEAYTRQHREARPALTSRLRFPDKPLRPIVNMDDYVYGA 642
		Qy	633 RALGRKRQAOHFTORLKLTFSMINLYERTKPHLMSGVSLGMNDIYRTWAFVLRVRALDQ 692
		Db	643 RTFRRBKRBRLTSRKAFLSVLNTERARRPLGLIASVGLDDIHTRAWTFVLRVRAQDP 702
		Qy	693 TPRMYFVKADTVGAYDATAFQGKLVVBVYANMIRHSESTYCIROYAVRDRDISQGYIKSFRR 752
		Db	703 PPELIVFVKDVTGAYDTIQDRLTVIASIK-BQNTYCVRYAVQKAAGHVTAKFKS 761
		Qy	753 QVTTISLDOPYMGQFLKHQSDASALNSVVIBOSISMNESSSSLEDFPLHLRHSVVK 812
		Db	762 HVSTITDQPMRQFVAHQQT--SPLRDAVITBQSSSLNEASGGFLDFVLFPMCHHAVR 819
		Qy	813 IGDRCYTOCGIPQGPOSSLTLLCSLCFGMENKLFABYORDGLLRFVDDFLLYVTPHLQD 872
		Db	820 IRGKSYVQCGIPQGPOSSLTLLCSLCFGMENKLFABYORDGLLRFVDDFLLYVTPHLQD 879
		Qy	873 AKTFELSTLHYGPEYGMINLQKTVVNPFVBPGLGGAQYQLPDPAHCLEFWCGULLDQT 932
		Db	880 AKTFELSTLHYGPEYGMINLQKTVVNPFVDEAUGGATFQVMRAGLFPWCGULLDQT 939
		Qy	933 LEVFDYSGYAQTTSIKTSLTQSVPKAGITMRKLLSVRLKCHGLFLDQVNSIQTYC1 992
		Db	940 LEVQDYSYSTARTSRASTFNRFKAGMRMRRCLFGVRLKCHSLFLDQVNSIQTYC1 999

Claim 2: Fig 2: 76pp: German.

XX This sequence represents a novel human catalytic telomerase sub-unit.

CC (hTC). This protein can be used in screening assays to identify modulators of telomerase and to treat or inhibit cellular disorders, death, defects and/or other pathological processes involving telomerase, particularly cancer and ageing (also suitable for this are agents that stimulate, inhibit or mimic the activity of the subunit). Antibodies particularly in neoplastic cells and may be expressed *in vivo*. Antibodies and fragments of the protein, used as probes or primers, are used to diagnose telomerase-related conditions (especially neoplasia) by (i) detecting abnormal levels of the subunit protein in body fluids or tissues or (ii) by measuring the amount of the encoding nucleic acid.

CC Expression of the nucleic acid encoding the subunit mRNA is confined to tumour cells, in contrast to the ubiquitous expression of the telomerase RNA subunit.

Qy	993	NIYKIFLQLQAYRFHACVIQLPFDORVRKNTTPEGLIISQASCCYAIUKVKNPGMTIKAS	1052	Matches 719; Conservative 122; Mi matches 260; Indels 52; Gaps 13;	
Db	1000	NIYKILLQLQAYRFHACVQLPFTIQQWNKNPTFFRVISDTASLCYSTILKAKNAGMSLGAK	1059	Qy 1 MTRAPRCPAVRSILLRSRYREWPLATVRRRLGPEGGRLLVQPDPCYRTTLVACQCLVCMHW 60	
Qy	1053	GS--FPPEAAHHLCYAQAFLLKAHSYTYKCLGLPLATAQKULCRKPEATMUTLKAAG	1109	Db 1 MTRAPRCPAVRSILLRSRYREWPLATVRRRLGPEGGRLLVQPDPCYRTTLVACQCLVCMHW 60	
Db	1060	GAAGPLPSEAQNUCHAQAFKLTRHRTTYVPLIGSLRTAQTLSRKPLGTITALEAA	1119	Qy 61 GSOPPPADLSFHOVSILKELYARVYORLCEERNERYLAFGPEELNEARGGPPMAFTSSVR 120	
Db	1110	DPAALSTDFTOTILD 1122		Db 61 DARPPPAAPSPQRQSVCLKELYARVYORLCEERAKVNLAFGFLDQGARGGPPEAFTSSVR 120	
Qy	1120	NPALPSDFKILID 1132		Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db				Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
RESULT 9				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
ID AAY288881		standard; protein; 1132 AA.		Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
AAY288881:				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
DT 17-JAN-2000		(first entry)		Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
DE Human telomerase reverse transcriptase protein.				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
KW Human telomerase reverse transcriptase protein; hTRT; telomerase; hEST2;				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
KW catalytic protein component; cell proliferative capacity; DNA primer;				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
KW telomerase substrate; telomeric DNA synthesis; cell immortality;				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
KW neoplastic phenotype; diagnostic application; prognostic application;				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
KW telomerase related condition; cancer therapeutic agent;				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
KW telomerase expression; telomerase activity.				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
OS Homo sapiens.				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
FH Key Location/Qualifiers				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Misc-difference 608				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
FT /note= "Corresponds to cac codon"				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
PN W09950279-A1.				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
PD 07-OCT-1999.				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
PF 31-MAR-1999;		99WO-US007160.		Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
PR 31-MAR-1998;		98US-00052919.		Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
PA GERON CORP.				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
PA (UYTE-) UNIV TECHNOLOGY CORP.				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
PI Andrews WH;				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
DR WPI: 1999-610834/52.				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
DR N-PSDB, AA208150				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
PT Antisense polynucleotides for human telomerase reverse transcriptase used				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
PT for diagnosing or treating cancer.				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
PS Claim 2; Fig 2; 31pp; English.				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
CC The present sequence is human telomerase reverse transcriptase protein.				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
CC This is the catalytic protein component of telomerase and is also				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
CC referred to as hEST2. hTRT has the ability to extend a DNA primer that				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
CC functions as a telomerase substrate for telomeric DNA synthesis. This				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
CC correlates with cell proliferative capacity, cell immortality, and the				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
CC development of a neoplastic phenotype. Human TRT antisense				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
CC oligonucleotides are useful for diagnostic or prognostic applications to				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
CC telomerase related conditions, including cancer. They are also useful as				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
CC therapeutic agents, for inhibition of telomerase expression and activity				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
XX Sequence 1132 AA;				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Query Match 59.4\$; Score 3505; DB 2; Length 1132;				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Best Local Similarity 62.4\$; Pred. No. 0;				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
DB 1000 NIYKFLQLQAYRFHACVQLPFDORVRKNTTPEGLIISQASCCYAIUKVKNPGMTIKAS 1052				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
DB 1000 NIYKFLQLQAYRFHACVQLPFTIQQWNKNPTFFRVISDTASLCYSTILKAKNAGMSLGAK 1059				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 1 MTRAPRCPAVRSILLRSRYREWPLATVRRRLGPEGGRLLVQPDPCYRTTLVACQCLVCMHW 60				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 1 MTRAPRCPAVRSILLRSRYREWPLATVRRRLGPEGGRLLVQPDPCYRTTLVACQCLVCMHW 60				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 61 GSOPPPADLSFHOVSILKELYARVYORLCEERNERYLAFGPEELNEARGGPPMAFTSSVR 120				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 61 DARPPPAAPSPQRQSVCLKELYARVYORLCEERAKVNLAFGFLDQGARGGPPEAFTSSVR 120				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Db 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180	
Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACALYLYPPSCAYQVCSCPLYQICA 180				Qy 121 SYLINTVETLRSVGMILLISRGDDLVYLALLACAL	

Qy	1053 GS---PPPEAAHMLCYQAFLIKLAHSVYTKCJGLPRTAQKLUJCRKLPEATMTILKA 1109	61 GSOPPADLSPHOVSISLKEVLVARVVRQLCERNRNRVIAFGFBLINEARGGPMAPFTSSVR 120
Db	1060 GAAGPLPSAVQWNLCHQAFLIKLTHRVTVPILLSRQTLTALEAKA 1119	61 DARPPAAPSFRQSCLKEVARYLQRICERGAKNVLAFGPAIDLGRCGPPEAPTTSVR 120
Qy	1110 DPALSTDPTQTLID 1122	121 SYLPNTVIETLRVSGAMMILLSRVGDDLVYLIAHCALYLYVPPSCAYOVCGSPLYQICCA 180
Db	1120 NPALSDPTQTLID 1132	121 SYLPNTVIETLRVSGAMMILLSRVGDDLVYLIAHCALYLYVPPSCAYOVCGSPLYQICCA 180
RESULT 10		181 TTDIWPVSASYTRPVPGRNFTNLRFLOQIKSSRQZAKPLALPSRCTKHLISLTSTS 240
ID AAY2090	AYY2090 standard; protein; 1132 AA.	181 ATQARPPHAS-GPRRLG-----CERAMNHVSREAGVPLGLPAPGARRGGSASRS 231
XX AC AAY2090;		241 VPSARKARCTYPVPRVEEGP-----HRQVLPTPSGKSW-VPSARSPEVTAERDLSKK 292
XX DT 17-JAN-2000 (First entry)		232 LPLPRPRGAAPPERRPVGQCSWAHPOTRTGPSDRGFCVSPAR----PAEATSLR 286
XX DE Human telomerase reverse transcriptase (hTRT).		293 GKVDLSLS-S-GSYCCKHKPKSSTSLLSPRQNAFOLRP-FILETRHFLYSLRGDGQERLNPSF 350
XX DB		287 GALSCTRSHPSVRQHAGPPSTSRRPWPDTCPCCPVYAAETRHFLLYSSGD-KEQLRPSF 345
XX KW Telomerase reverse transcriptase; human; hTRT; cell proliferation; cancer.		351 LLSENQPNLTGARLVEIIFLGSRPTGSPLCRTHRLSRRYQWQRLPFCQLLYVHABCOY 410
XX OS Homo sapiens.		346 LLSSURPSLUTGARLVEITFLGSRPPMPSTPRLRPLPRLGHNHQCPY 405
XX PN W09950386-A2.		411 VRLLRSHCRFRTANQVTDAL-----NTSPPHMDLRLASSPQWY 452
XX PD 07-OCT-1999.		406 GVLLKTHCPLRAA--VTPAAGVCAAREPQGSVAAPEEBDTDPRLVQLRQHSSPKQVY 462
XX PP 31-MAR-1999; 99WO-US007097.		453 GFLRACLCKVVSASLWGTTRHNERRFKQNLKKFFKSLGKTYGKSLSOBLMWKMKVBDHWR 512
XX PR 31-MAR-1998; 98US-00052864.		463 GPERACLRRUVRUPPSLWGSRHNERKFPLNTKCFISLGKHAKLSSOBLTWKMSVRDCAWLRR 522
PR 03-AUG-1998; 98US-00123354.		513 SPGKDPRVPAAEHRLRERILATEFWLMDTYYVQILRSPEVITESTFOKNRLFFYRKSWS 572
XX (GBRO-) GERON CORP.		523 SPGTCVPAAEHRLRERILAKFLHMLMSYVVBULLRSPEVTTETTFOQNRLFFYRKSWS 582
XX PI Morin GB;		573 KLOSIGVROHLERYVRRLREUSQBEYRHDQTWLAMPICLRLPKPKNGLRPIVNMYSMGT 632
XX DR; 1999-610842/52.		583 KLOSIGIROLKRVQVLRESEAATYQREARPALTSRIPRIPKPDGLRPIVNMNDYVVER 642
XX N-PSDB; AZ202979.		633 RALGRKAOAHFTORKLTLFSMNLXERTYKPHLMSGSVIGMDIYTRTAFLVRLRDLQ 692
XX PT New catalytic polypeptide and polynucleotide, useful for increasing catalytic activity in a cell.		643 RTFREKRAERLTSRVKALPSVNLNTARRPGLGASVLGDDIIRHAMRTFVLVRQAQP 702
PS Claim 13; Fig 1; 24pp; English.		693 TPRMFYKVADTVGAYDAIFQGKLVVBBVANMRHESSTCIRQAVYVRADSQGVTKSPR 752
XX CC The present sequence represents human telomerase reverse transcriptase (hTRT). Human telomerase is a target for diagnosing and treating diseases relating to cell proliferation and senescence, such as cancer, or for increasing the proliferative capacity of a cell. A claimed method for increasing the proliferative capacity of a vertebrate cell, especially a human or other mammalian cell, involves introducing into the cell a recombinant hTRT polynucleotide encoding an hTRT variant in which residues 192-323, 192-271, 200-323, 192-271, 200-271, 222-323, 415-450, 192-323 and 415-450, or 192-271 and 415-450 of the present sequence are deleted. A claimed method of preparing recombinant telomerase involves contacting a recombinant hTRT deletion mutant (as above) with a telomerase RNA component such that the 2 proteins associate to form a complex capable of catalysing the addition of nucleotides to a telomerase substrate. A claimed method for reducing telomerase activity in a cell involves introducing a recombinant polynucleotide encoding an hTRT variant having a deletion of amino acids 192-450, 560-565, 637-660, 638-660, or 1055-1071 of the present sequence.		703 PPELYFVKYDVTGADTFDQDRLTVEIASIK-PNQTYCVRYAVQKAHGHYRKAFPS 761
XX SQ Sequence 1132 AA;		753 QVTTISDLOPYMGQFLKHQDSDASALRNSSVVISQISSNESSLFDPLHPLRHSVVK 812
CC		762 HVSTLTDQPYMQRQVFAHQIQT--SPLRDAVVEQSSSLNEASQCLFDYFLRMCHAVR 819
CC		813 IGDRCYTOCGIPQSSSLSTLCSCFGDMENKLFAEVORDGLLRFFVDFPLLTTPHLDQ 872
CC		820 IRGKSYVQCGIPQSSLSTLCSCFGDMENKLFAIRDRGLLRFLVDFLLTPHLDH 879
CC		873 AKTFPLSTLVHGPYPEYGMINLQKTVNFVYBPGTIGGAPYQLPWHCLPFWCGLILDPTQ 932
CC		880 AKTFPLRTLVGPEGVNLRKTVNFPVBDALGGTAFVQMPAHGLFWCGLILDTRT 939
CC		933 LEVFDYSGAQTSKTSKTSLTPQSYVKAGKTMRNKLSVRLKCHGFLDLQVNSLQTVCI 992
CC		940 LEVQDYSSSTARTSRASTLTFNRGTFKAGRMRRCLFGVIRLKCHSFLDLQVNSLQTVCI 999
CC		993 NIYKFLLOQYRFHCVIQLPFDQVRLNLTTPFLGISSOASCYVAILKVNPNMTLKA 1052
CC		1000 NIYKILLQYRFHCVIQLPFPHQWQWNPFTPELRVTSITASLCSYVILKAGNAGISLGK 1059
CC		1053 GS---FPPBAAHMLCYOAFLIKLTHRVTVPILLSRQTLTALEAKA 1109
Qy	1 MTRAPRCPAVRSLLRSRREVWPLATFVRLLGPEGRLVQGDPLKTYLVAQCLVCMHW 60	1060 GAAGPLPSAVQWLCQAPFLKTRHRVTVPLUGSRLTAQTLSRKLPOTTIAMEAAA 1119
Db	1 MTRAPRCRAVRSLLRSRHYREVPLATFVRLLGPEGRLVQGDPAAPRFLVAQCLVCPW 60	

Qy	181	TTDIWPSVSASYRPRTRPVGRNFTNLRFLOOKKSSRQEAKPKLALPSRGTYKHLISLTSTS	240
Db	181	ATQARPPPHAS-GPRRLG-----CERAWNHSVREAGVPLGIAPGARRGGSSAARS	231
RESULT 11			
AAY43621	1110	DPALSTDFOTILD 1122	
ID	1120	NPALPSDFKTLID 1132	
XX		AAY43621 standard; protein; 1132 AA.	
AC			
XX			
XX	26-JAN-2000	(first entry)	
XX			
DE		A human telomerase reverse transcriptase (TRT) polypeptide.	
XX			
XX		Human; telomerase reverse transcriptase; TRT; T lymphocyte activation; dendritic cell; telomerase activity; cancer cell; proliferating cell; immunological destruction; telomerase; cancer; proliferation disease.	
XX			
OS		Homo sapiens .	
XX			
PN	W09950392-A1.		
XX			
PD	07-OCT-1999.		
XX			
PP	30-MAR-1999;	99WO-US006898.	
XX			
PR	31-MAR-1998;	98US-0112006P.	
XX			
PA	(GERO-) GERON CORP.		
XX			
PT	Gaeta FCA;		
XX			
WPI	1999-610845/52.		
DR	N-PSDB; AAZ30154.		
XX			
PT	Biliciting an in vivo immune response for prevention and treatment of cancers.		
XX			
PS	Claim 3; Fig 1; 26pp; English.		
XX			
CC	The present sequence represents a human telomerase reverse transcriptase (TRT) polypeptide. The protein is used in the method of the invention.		
CC	The specification describes a method for activating a T lymphocyte, comprising contacting the T lymphocyte with a dendritic cell that expresses a TRT peptide in the context of a MHC class I or MHC class II molecule. The protein causes induction of an in vivo immunological response to telomerase activity. Cancer cells are characterized by expression of endogenous TRT gene and the presence of detectable telomerase activity. Therefore, by eliciting a specific immune response to TRT or to TRT-expressing cells, it is possible to selectively target proliferating cells for immunological destruction. The method is used for eliciting an in vivo immune response to telomerase by activating a T lymphocyte, and is useful for prevention and treatment of cancers and other proliferation diseases/conditions		
XX			
SQ	Sequence 1132 AA;		
Qy	59.4%; Score 3505; DB 2; Length 1132;		
Best Local Similarity	62.4%; Pred. No. 0;		
Matches	Conservative 122; Mismatches 260; Indels 52; Gaps 13;		
Db	1000 NIVKILLQIQAQRHACTYQLPPDQVRKRNLTFFGIGIISQASCCYALRKVNPMKIKAS	1052	
Db	1000 NIVKILLQIQAQRHACTYQLPPDQVRKRNLTFFGIGIISQASCCYALRKVNPMKIKAS	1059	
Qy	1 MTRAPRCAVSLLRSRYREVWPLATEYFRLGPGRGLYQPGDPKIVRTLVAQCLVCMHW	60	
Db	1 MTRAPRCAVSLLRSRYREVWPLATEYFRLGPGRGLYQPGDPKIVRTLVAQCLVCMHW	60	
Qy	61 GSQPPADLSFGQVSSLLKLYARVQRICERIERNVLAFFBFLNEARGPPMAFTSVR	120	
Db	61 DARPAAAPSPQVSCLKEVAVLQRICERGAKNVLAFFGFLALDDGRRGPBAFTSVR	120	
Qy	121 SYLPNTVLETRVSGAMWLLSRVGDDLVVLAHCAVLYIYPPSCAYQCGSPLYOICA	180	
Db	121 SYLPNTVLETRVSGAMWLLSRVGDDLVVLAHCAVLYIYPPSCAYQCGSPLYOICA	180	
Qy	121 SYLPNTVLETRVSGAMWLLSRVGDDLVVLAHCAVLYIYPPSCAYQCGSPLYOICA	180	
Db	121 SYLPNTVLETRVSGAMWLLSRVGDDLVVLAHCAVLYIYPPSCAYQCGSPLYOICA	180	

XX	AAY26580;	351	LLSNLQPNLTGARRLVEIIFLGSRRTSGPLCRTLRLSRRYWMRPFQQLLYNHAECOY	410
AC		346	LLSLRPSITGARRLVETIFLGSRPMGTPTRLPRLPORYQMRPLFLELGNNHQCPY	405
DT	13-SEP-1999 (first entry)	411	VRLRSHCRFRFTANQQTDAL-----	452
XX	Human telomerase reverse transcriptase (hTERT) enzyme.	412	NTSPPHFLMDLLRHSSPWQVY	452
DB		406	GVLILKTHCPLRAA--VTPAGVCAREKPGSVAAPEBDTDPRRLVOLRHOSSPWQVY	462
KW	Telomerase reverse transcriptase; TERT; mouse; telomere length assay; telomerase-mediated DNA replication; human.	463	GFLRACLCKVVSASLWGPTRHNERPFRKLKKPISLGKYGKLSLQEELAKMVKYEDCHNTRS	512
OS	Homo sapiens.	463	GFLRACLCKVVSASLWGPTRHNERPFRKLKKPISLGKHYAKLSQLBLTKMSVRDCANLRR	522
PN	WO9927113-A1.	513	SPGRDTRPAEHRLERILATFLWLMDTYVOLLRSPPYTESTFQRNRLPYRKSTWS	572
PD	03-JUN-1999.	523	SPGYGCVPAEHRLERILATFLWLMSVYVLLRSPPYVETTFQGNRLPYRKSTWS	582
XX	PA (GERO-) GERON CORP.	523	SPGYGCVPAEHRLERILATFLWLMSVYVLLRSPPYVETTFQGNRLPYRKSTWS	582
PP	25-NOV-1998; 98WO-US025211.	573	KLQSGIVROHLERYVRRLRELSEQQEVRRHODTWLAMPICRLRFPKPGLRPIVNMYSNGT	632
XX	PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.	583	KLQSGIVROHLKRVQLRBLSEAEVRQHBRARPALTSRLRIFPKDGLRPIVNMYYVGA	642
PR	26-NOV-1997; 97US-00979742.	633	RALGRKKAQHFFPQLKPSMLNEYEPYKPHLMGSSVIGANDIYRTWTRAFYLRVRALDQ	692
PR	16-MAR-1998; 98US-00042460.	643	RTPFREKRAEURLSRVAKLFSVNLNEYEARRPGHLGASTGLDDTHRATRTFVLRVRAOPD	702
XX	PI Morin GB, Allsopp R, Depinho R, Greenberg R;	693	TPTMYFVKADTVGAYDAFPQGKLUVEVANMIRHSESTYCIRQAVVRDRDSQGVTHSKFR	752
DR	WPI; 1999-347722/29.	703	PPEIYFVKUDVTGAYDTIPQDLRTEVIAIIK-PONTICVRRAYVQKAAGHIVRKAVS	761
XX	PT Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and nucleic acids.	753	QVTTLSDIOPYMGOFKLHQDSDASALRNSSVIEQSISMNESSSSLFDFHLPLRSVVK	812
PT	XX Disclosure: Fig 3; 135PP; English.	762	HVSFLRDQPMQFAVHLQET - SPLEDAVVIEQQSSSLNEASSGLFDVPLRMCHAVR	819
PS		813	IGDRCYCTOCOGIPGGSSSTLCLCGDMENLFLAYTGDGLLRFYDFLFLVTPHLDQ	872
XX	CC The invention relates to a mouse telomerase reverse transcriptase (mTERT) enzyme. Compositions containing mTERT can be used in telomere length assays. Isolated mTERT is useful as an immunogen for the production of monoclonal or polyclonal antibodies. The method is useful for assessing the degree of purification and identification of new mTERt species, such as an mTERT allele, homolog or isoform, or to screen for modulators (antagonists and agonists) of telomerase-mediated DNA replication. Other telomerase enzymes such as human TERT (hTERT). The present sequence represents a human TERT enzyme.	820	IRGKSYVQCGIPGGSSSTLCLCGDMENLFLAYTGDGLLRFYDFLFLVTPHLDQ	879
CC		873	AKTPLSTLVHGVBYGCMINLQKTVNNEPVPGTLLGGAPYQOLPAHCFLPWCGLLDPQT	932
CC		880	AKTPLSTLVHGVBYGCMVNLRCVUVNPNEVEDDEALLGTAFVQMPAHGLFPWCGLLDPQT	939
CC		933	LEVFDYSSQYQTSIKTSLSITQSVPKAGTMRNLLSVRLKCHGFLDQLQNSLQTVCJ	992
CC		940	LEVOISDYYSSYARTSIRASUTPNRGPKAGRNMRKLFQVLRKCHSFLDQVNSLQTVCJ	999
XX	Sequence 1132 AA;	993	NIYKFLIQLQYRFLAFCYQVLPQFLDPRVKNLTFFFGIIISQASCYTLKVNPNMTLKS	1052
SQ	Query Match Score 3505; DB 2; Length 1132;	Db	1000 NIYKFLIQLQYRFLAFCYQVLPQFLDPRVKNLTFFFGIIISQASCYTLKVNPNMTLKS	1059
Best Local Similarity 62.4%; Pred. No. 0; Mismatches 719; Conservative 122; Indels 260; Gaps 13;	Qy	1053 GS---PPPEAAHWLQYQAPLKLAAHSVTYKCLQPLTAQKQLCRKLPEATMTLKA	1109	
Matches 1109	Db	1060 GAAGFLPSEAVONLCHQAPLKLTRHRTYVPLIGSLRTAQTL-SRKLPGTTLTALEAAA	1119	
Db	1 MTRAPCPAVPSLRSRYREYPLATEVRLGPEGPGRRLVQGDPKLYTFLVVAOCILVCMW 60	Qy	1110 DPALSTDFGTILD 1122	
Db	1 MPRAPCRAVSLRSHREYPLATEVRLGPEGPGRRLVQGDPAPAFRALVAQCLIVCPW 60	Db	1120 NPALPSDFKTILD 1132	
Qy	61 GSQPPPADLSTHQVSSLKELYARIQLCERNERNVTLAFGELLNEARGGPPMAFTSSVR 120	RESULT 13		
Db	61 DARPPPPAPSPTQVSKCKEYAVBLQRLCAGPALLDQGARSPPEATTTSR 120	AAG64859		
Qy	121 SYLPNTVETLRLSGAWMILLSRGDDLLYUULLAHCALYLLVPPSCAYQVCGSPLYQICA 180	Db	21-SEB-2001 (first entry)	
Db	121 SYLPNTVETLRLSGAWMILLSRGDDLLYUULLAHCALYLLVPPSCAYQVCGSPLYQICA 180	XX	XX	
Qy	181 TTDIWPSVASYRPTPVGRAFTNLREFLQOKTSKSSRQEAKPLALPSRGTKRHSLSTS 240	XX	XX	
Db	161 ATQARPPHAS-GPRRLG-----CERAWHNSYREAGVPLGAPRGRRGSASRS 231	XX	XX	
Qy	241 VPSAKKARYCYPYPRVEGPP-----HRQVLPTPSKSKW-VPSPARSPVEPTAEDLSK 292	DE	Heart muscle cell differentiation related protein SEQ ID NO: 31.	
Db	232 LPLPKPRGAAPEPRTPVQGSGWHPGRTRGPSPDRCVSPVSP-----PAEPATSLS 286	XX	KW Heart muscle cell; human; cell differentiation; heart disease.	
Qy	293 GKVDSLISLGSVCKRKHKPSSSTSLLSPRQNAFQQLP-FLETTRFLYSGDQGBBLNPSF 350	OS	XX Homo sapiens.	
Db	287 GALSGTRHSHPSVGRHHAGPBPSTSKRPRPNDTPCPBPVVAETKHFYSSGD-KEQIRPSP 345	PN	WO200148151-A1.	

cell types other than cardiomyocytes; (4) drug compositions promoting the formation of heart muscle and regeneration of heart tissue which contain the cells; (5) a method for the production of antibodies which recognise the cells; especially antibodies which recognise a surface antigen on the cells; (6) a method for screening factors which promote the proliferation of the cells; (7) a method for immortalising the cells by expressing telomerase in them; (8) drug compositions for the treatment of heart disease which contain the immortalised cells; and (9) cell-free supernatant from the culture of the cells and its use in promoting their differentiation into cardiomyocytes. The cells are used in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction and in the study of cardiomyocyte differentiation. AAB44351 to AAB4409 and AAB9915 to AAB9935 represent sequences used in the exemplification of the present invention

xx

Sequence 1132 AA;

Query Match 59.4%; Score 3505; DB 4; Length 1132;
Best Local Similarity 62.4%; Pred. No. 0;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

Qy 1 MTRAPCRAVSRLRSRREVPLATFVRLGPEGRVLQEPDVKLYRTLVHQCLVCMHW 60

Db 1 MPRAPCRAVSRLRSRREVPLATFVRLGPEGRVLQEPDVKLYRTLVHQCLVCMHW 60

Qy 61 GSOPPAPALSFHQVSSLKEVLAQVQLCERNERNVTLAEGFELLNEARGGPMAFTSSVR 120

Db 61 DARPRAAPSPRQVSCLKEVLAQVQLCERNERNVTLAEGFALLDGRRGGPPEAFTSSVR 120

Qy 121 SYLPNTVLTLETRSGAWMILLSLRGDDLVYLIAHCAVLYLVPSCAYQVCCSPLYQICA 180

Db 121 SYLPNTVTDALRGSGANGLLLRVGDVLLVHLLARCAFLVLYLVPSCAYQVCCSPLYQICA 180

Qy 181 TDIWPSVSYASASTRPTPVGRNPTNLRLPQQTKSSSRDQAKPELPSRGTRGHLSLTSTS 240

Db 181 ATOARPPIHAS-GPERRIG-----CBRANNHSVREAGVPLGLPAGARRGGAAARS 231

Qy 241 VPSAKKARCYPPVREBGP-----HRQVLPTPSGKSW-VPSPARSPVEVTAEKLDSK 292

Db 232 LPLPKRPRGAAPEPRTPTVGCGSWAHPGRTGPGSDRGFCVSPAR-----PAEATSLE 286

Qy 293 GKVDLSLS -GSVCKKHPKSSSTLSPRQNAFQLRP-FIETPRHFLYSRGDCQERLNPsf 350

Db 287 GALSGTRHSHPSVGRQHAGPSTSRSPRWDTPCPVYAAETKHPLYSGD-KEQLRPSf 345

Qy 351 LJSNLQPLTGARRLVETIFLGSRPTSGPLCRTHRSLRYYQMRPFLFOQLVNHAEQY 410

Db 346 LJSSLRPLTGARRLVETIFLGSRPTSGPLCRTHRSLRYYQMRPFLFOQLVNHAEQY 405

Qy 411 VLLRSHCRFRANQVTDAL-----NTSPPHMLDLRHSSPWQYQ 452

Db 406 GVLLKTHCPLRRA-- -VTPAAGYCAREPQGSAVAPEEDTDPRRLVQLLRQHSSPMQVY 462

Qy 453 GPFLRACKVVASLWGTNRNBRFFKNLKRFPSLKGKUSLQEIMWKMVKEDCWLRs 512

Db 463 GFYTRACRLLRVPPGLNGSRHNERFLANTKETTSLGKHAQLSQELTWSMURDCAWLR 522

Qy 513 SPKDRIVEAERLRLRERLRLATEFFWLMIDTYVYLLRSEFYTESTFONRNFYFYSQWS 572

Db 523 SPEGCVAAEHLRLREEELAKPFLHWMNSVYVLLRSEFYTESTFONRNFYFYSQWS 582

Qy 573 KLSQIGYVQHLERVLRLSQQEBVRHICDTWLAMPICLRLPKENGLRPTYNMSMGT 632

Db 583 KLSQIGYVQHLERVLKRVQRLRSEAEVROTEARPALLTSLRFPKPDGLRPTVNMDTVVGA 642

Qy 633 RAIGRKKAQHFQRKLTFMSMANYERTKPHILMGSVYGRNDIYTRWRAFTLVRALDQ 692

Db 643 RTRPRREKAERLTSRVKULPSVLYERARRPGLGASVGLDDIIRHRAWTFLVRVRAQDP 702

Qy 693 TPEMYFVADYTCGAYDAIPQGLKVEVYANMTRHSESTCROYAVYRDSOCQVHKSFRR 752

Db 703 PPELYFVKDVTCGAYDTIPQDLRTEIASIIK-PQNTYCVRYAWOKAAHGVRLKA KS 761

Qy 753 QVTTLSDLOPQYQFQFLKHLQPSDASALIRNSVYIEQSISNESSSSLSDFFLHPLRHSVVK 812
Db 762 HVSTLTDLQPMRQFVHLQQT--SPARDAVIQLQSSLNASSGLDVFVLFPMCHAVR 819

Qy 813 IGDRCYTQCQGIPOGSSLSTLCSLCFGDMENKLFABEVORDGLLRFVDDPFLYTPHLDQ 872
Db 820 IRGKSTVQQCQGPQGSLSTLCSLCYGDMEALKFAGIRRDGLLRLVDDPFLVTPHLTH 879

Qy 873 AKTPLSTLVRGVPEYQGMINIQKTVNPNVBPGLGAAQVPLAHCLPMPICLGLDDQT 932
Db 880 AKTFPLRTLVRGVPEYCCVNLRKTVNPFVDEALGTAFVQMPAGLFPMPGGLUDTRT 939

Qy 933 LEVFDYSGTAQTSKTSLTFQSVPKAGTMRNKQLSVLRKCHGLFLDLOVNSLQVCI 992
Db 940 LEVQSDISYSTARTSIRASLTPTNPGFAGRNNRRCLEGVRKCHSLFLOVNSLQVCT 999

Qy 993 NIYKIFLQOAYRPHACYTIOLPFDQYRKRNLTFELGTTISSOASCYTAILKVKNPGMTLKAS 1052
Db 1000 NIYKILILQOAYRPHACYQLQPHQOQWKNPFPFLRVISDPLCSLTSILKARNAGSILGAK 1059

Qy 1053 GS-- -PPBEAHWLCYOAFLKLAHSVYKCLLGPLRTAQKLRLPLRATMTIKAAA 1109
Db 1060 GAAGPUPSEAQWHLQOAFPLKLTHERVTYVPLLSURTAQTQLSRKLPGTLTVAEAAA 1119

Qy 1110 DPALSTDPTQTLID 1122
Db 1120 NPALSPSKTLLD 1132

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